

IN THE CLAIMS

1-3. (canceled).

4. (currently amended) A method for ~~reducing sequencing errors by sequencing, recovering and resequencing a single stranded template nucleic acid, the method comprising:~~

- (a) forming an array of immobilised single-stranded template nucleic acid molecules wherein the density of immobilised single-stranded template nucleic acid molecules is 10^6 - 10^9 different template sequences per cm²;
- (b) determining the sequences of the immobilised single-stranded template nucleic acid molecules by synthesising a complementary copy of the template sequences, thereby performing a first round of sequencing;
- (c) removing the complementary copy of the template sequence synthetic strand; and
- (d) performing a second round of sequencing of the immobilised single-stranded template nucleic acid molecules, and wherein comparison of
- (e) comparing the first and second rounds of sequencing of each immobilized single-stranded template nucleic acid molecule to confirm sequencing data reduces sequencing errors.

5-26. (canceled).

27. (currently amended) The method of claim 4, wherein the template nucleic acid molecules polynucleotides are attached to a double stranded anchor.

28 (currently amended) The method of claim 27 28, wherein the double stranded anchor comprises a self complementary hairpin.

29 (previously presented) The method of claim 27, wherein the double stranded anchor comprises a recognition site for a restriction endonuclease.

30 (previously presented) The method of claim 4, wherein the 10^6 - 10^9 templates are individually resolvable single molecules.

31 (previously presented) The method of claim 4, wherein the sequencing determination is carried out using cycles of incorporation and detection of fluorescently labeled nucleotides.

32 (previously presented) The method of claim 31, wherein the fluorescent nucleotides are detected using a microscope with total internal reflection based imaging.

33. (new) The method of claim 4, wherein said synthesizing a complementary copy of the template sequences comprises employing a polymerase enzyme to synthesize a complementary strand on the template strand one base at a time.